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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/067,649

DATE: 02/26/2002
TIME: 13:27:26

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\02262002\J067649.raw

ENTERED

3 <110> APPLICANT: Bristol-Myers Squibb Company
5 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY14, RELATED
TO THE
6 ORPHAN GPCR, GPR73
8 <130> FILE REFERENCE: D0118 NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/067,649
C--> 10 <141> CURRENT FILING DATE: 2002-02-05
10 <150> PRIOR APPLICATION NUMBER: US 60/266,525
11 <151> PRIOR FILING DATE: 2001-02-05
13 <150> PRIOR APPLICATION NUMBER: US 60/329,897
14 <151> PRIOR FILING DATE: 2001-10-16
16 <160> NUMBER OF SEQ ID NOS: 92
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2654
22 <212> TYPE: DNA
23 <213> ORGANISM: homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1286)..(2464)
29 <400> SEQUENCE: 1
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32 aggaagaatc ctgttcattt tcaacatttt agccatcctg gtgatagtga ttatggagggt 120
34 gtacaaatcg tgggccaaga tgagactgat gaccggcctg aatgtcccta tggaccatcc 180
36 tgttatagga agaatcccca gcacaagata gaatatagac ataatacgtt tccagtggaga 240
38 aatgttttag atgaagataa tgataatgtt gggcaaccca atgagtatga cctgaacgac 300
40 agctttctag atgatgagga agaagactat gagccaacag atgaagattc tgactgggaa 360
42 ccaggaaagg aagatgaaga gaaggaagat gtggaagagc ttttgaaaga agcaaaaagc 420
44 aaataatttc ccgcatcttc actcttcatc tccccaccct cttctggaca actcctgaca 480
46 ttctgtgata ttcagcattc accataaaca ttgcatgatt cagttctcct tgatatcttg 540
48 gtgcttgagc tcttctactg ttggcatcatt aggtcagcag gtgaacactc aggattgttt 600
50 ctcttctgtt agtagagcac caaaagacag ggtctggctc tgtcaccta ggcagagggc 660
52 aatggtacaa tcaccattga ctgcagtctc aaattcctgg gctcaagcaa tctctccgcc 720
54 tcagcttccc aagcagctgg gactacaggc atgccccacc atgtccaggg aatggtgtct 780
56 ggaccacagag aataactgga tcttcaagga aggaagagaa atcttcagaa gaacatggat 840
58 tttcccact ggtagttagt tgtctcttcc atatccagaa ataacttgaa cacgttagac 900
60 ggggccactg tgcatagtgt cctcccagga aaacgccaaag attctccaag acactttcat 960
62 atcctaagcc ctgttctgtt tgttcttggt tagtaaattg gcaaatttgg cagtacagaa 1020
64 gacatctcta acctgatgtc acaaagaatc atgtctggcc catacaaagt attctaacta 1080
66 accatgtaag ccactagaat gttaactaa tgctctggca ctgaggttta gaatggagct 1140
68 cagataccat accccaaaga tgctggcaga gacattctga ctcattaagg gagagctggc 1200
70 tgatagcaga gaggggtgac atcagccttg cagacattgc cctggggaat tctgagcagt 1260
72 gttgctcaca gcaccacctg gccag atg gag acc acc atg ggg ttc atg gat 1312
73 Met Glu Thr Thr Met Gly Phe Met Asp

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140 gga ttc cag aca gag cag atc cgc aag agg ctg cgc tgc cgc agg aag      2128
141 Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys
142                270                275                280
144 acg gtc ctg gtg ctc atg tgc atc ctc acc gcc tac gtg cta tgc tgg      2176
145 Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp
146                285                290                295
148 gcg ccc ttc tac ggc ttc acc atc gtg cgc gac ttc ttc ccc acc gtg      2224
149 Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val
150                300                305                310
152 ttt gta aag gag aag cac tac ctc act gcc ttc tac atc gtc gag tgc      2272
153 Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu Cys
154                315                320                325
156 atc gcc atg agc aac agc atg atc aac act ctg tgc ttc gtg acc gtc      2320
157 Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr Val
158 330                335                340                345
160 aag aac gac acc gtc aag tac ttc aaa aag atc atg ttg ctc cac tgg      2368
161 Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu His Trp
162                350                355                360
164 aag gct tct tac aat ggc ggt aag tcc agt gca gac ctg gac ctc aag      2416
165 Lys Ala Ser Tyr Asn Gly Gly Lys Ser Ser Ala Asp Leu Asp Leu Lys
166                365                370                375
168 aca att ggg atg cct gcc acc gaa gag gtg gac tgc atc aga cta aaa      2464
169 Thr Ile Gly Met Pro Ala Thr Glu Glu Val Asp Cys Ile Arg Leu Lys
170                380                385                390
172 taacccctg gactttgcaa agtttaaaca caaagcaggg tcctgtggac actgactagt      2524
174 gtgcttggat gcacatcaac ctggaacttt ttgtttgctg cagagggtaa agtaaatgga      2584
176 ccactctgtg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2644
178 aaaaaaaaaa                                     2654
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 393
183 <212> TYPE: PRT
184 <213> ORGANISM: homo sapiens
186 <400> SEQUENCE: 2
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193                20                25                30
196 Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
197                35                40                45
200 Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
201                50                55                60
204 Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn
205 65                70                75                80
208 Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
209                85                90                95
212 Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
213                100                105                110
216 Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
217                115                120                125

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220 Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
221      130                      135                      140
224 Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
225 145                      150                      155                      160
228 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
229                      165                      170                      175
232 Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu
233                      180                      185                      190
236 Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
237      195                      200                      205
240 Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
241      210                      215                      220
244 Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
245 225                      230                      235                      240
248 Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
249                      245                      250                      255
252 Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
253                      260                      265                      270
256 Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
257      275                      280                      285
260 Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
261      290                      295                      300
264 Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
265 305                      310                      315                      320
268 Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
269                      325                      330                      335
272 Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
273                      340                      345                      350
276 Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
277      355                      360                      365
280 Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
281      370                      375                      380
284 Glu Glu Val Asp Cys Ile Arg Leu Lys
285 385                      390
288 <210> SEQ ID NO: 3
289 <211> LENGTH: 355
290 <212> TYPE: PRT
291 <213> ORGANISM: homo sapiens
293 <400> SEQUENCE: 3
295 Tyr Gly Asp Tyr Asp Leu Pro Met Asp Glu Asp Glu Asp Met Thr Lys
296 1      5      10      15
298 Thr Arg Thr Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala
299      20      25      30
301 Gly Ile Met Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala
302      35      40      45
304 Leu Thr Arg Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala
305      50      55      60
307 Asn Leu Ala Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe
308 65      70      75      80

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310 Glu Met Asp Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His
311                               85                               90                               95
313 Val Leu Cys Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val
314                               100                               105                               110
316 Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile
317                               115                               120                               125
319 Val His Pro Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu
320                               130                               135                               140
322 Ile Ala Leu Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala
323 145                               150                               155                               160
325 Tyr Phe Ala Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys
326                               165                               170                               175
328 Ile Phe Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys
329                               180                               185                               190
331 Ser Tyr Phe Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val
332                               195                               200                               205
334 Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys
335                               210                               215                               220
337 Ala Val Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys
338 225                               230                               235                               240
340 Arg Arg Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val
341                               245                               250                               255
343 Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe
344                               260                               265                               270
346 Pro Thr Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val
347                               275                               280                               285
349 Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Val Cys Phe
350                               290                               295                               300
352 Val Thr Val Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met Met Leu
353 305                               310                               315                               320
355 Leu His Trp Arg Pro Ser Gln Arg Gly Ser Lys Ser Ser Ala Asp Leu
356                               325                               330                               335
358 Asp Leu Arg Thr Asn Gly Val Pro Thr Thr Glu Glu Val Asp Cys Ile
359                               340                               345                               350
361 Arg Leu Lys
362                               355
364 <210> SEQ ID NO: 4
365 <211> LENGTH: 393
366 <212> TYPE: PRT
367 <213> ORGANISM: Mus musculus
369 <400> SEQUENCE: 4
371 Met Glu Thr Thr Val Gly Ala Leu Gly Glu Asn Thr Thr Asp Thr Phe
372 1                               5                               10                               15
374 Thr Asp Phe Phe Ser Ala Leu Asp Gly His Glu Ala Gln Thr Gly Ser
375                               20                               25                               30
377 Leu Pro Phe Thr Phe Ser Tyr Gly Asp Tyr Asp Met Pro Leu Asp Glu
378                               35                               40                               45
380 Glu Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
381                               50                               55                               60

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:988 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:1006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:1014 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:1032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1040 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:1052 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:1064 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:1076 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:1088 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:1460 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:88
L:1473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:89
L:1486 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:90
L:1499 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:91
L:1512 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:92